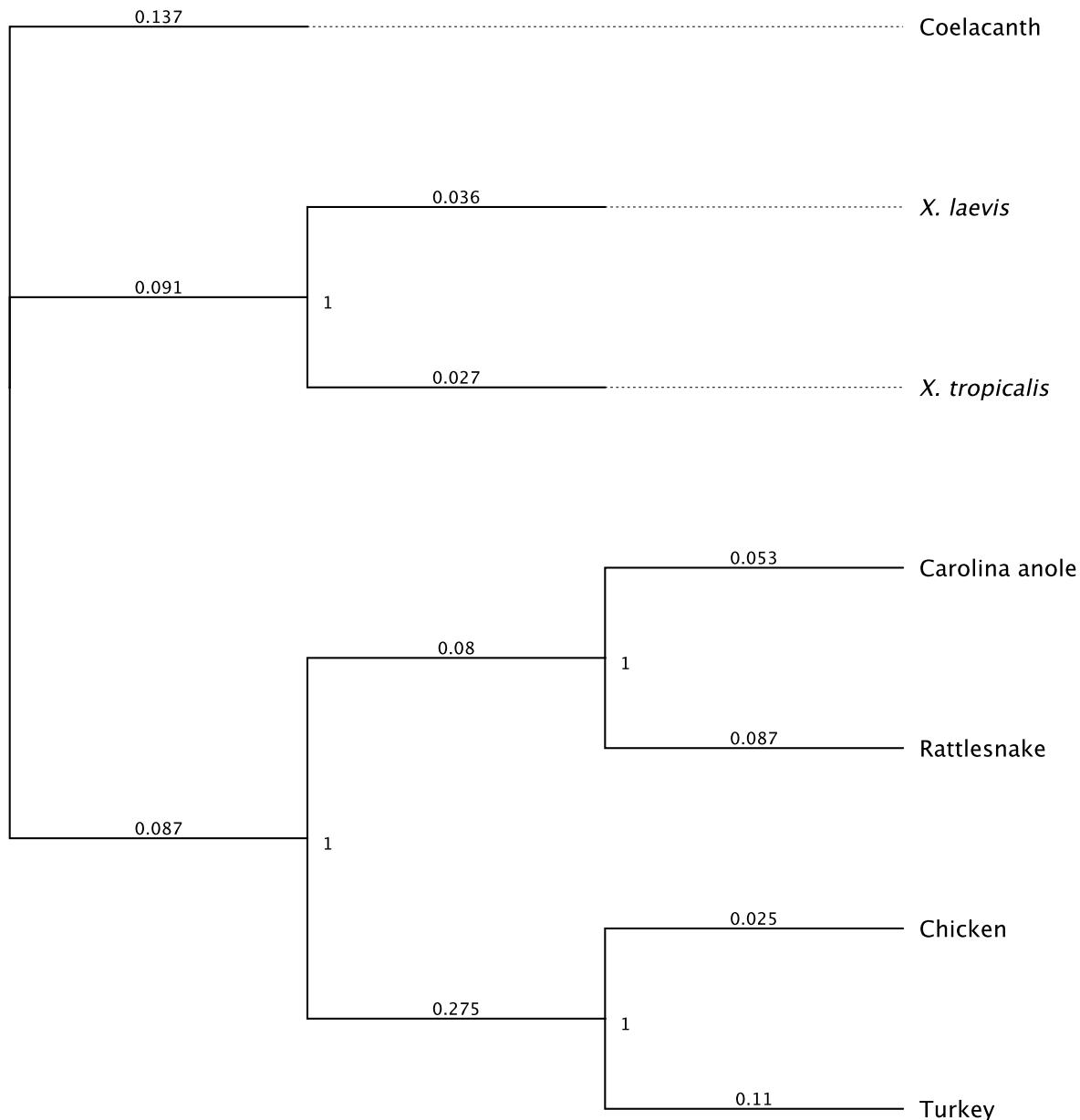
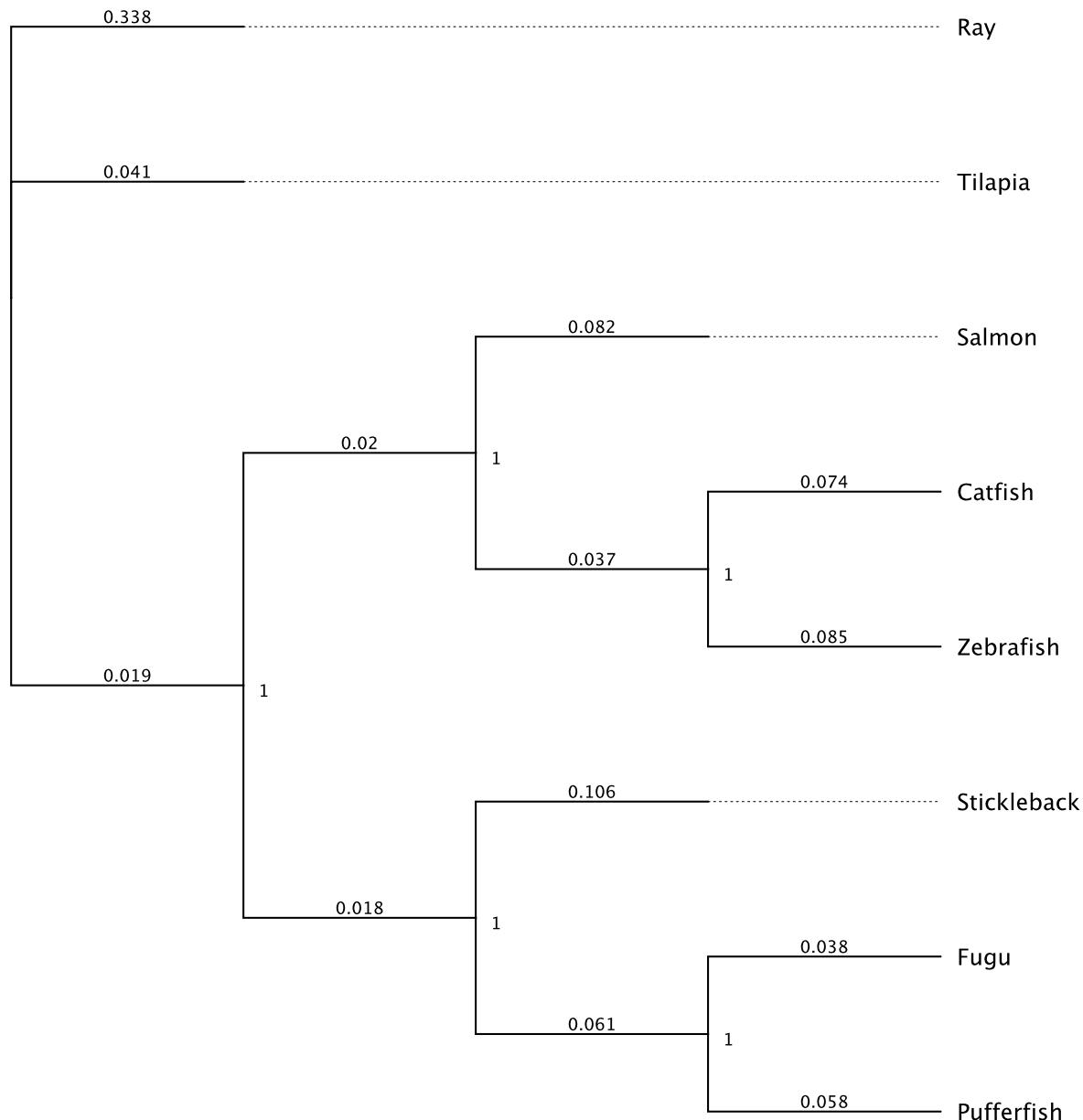


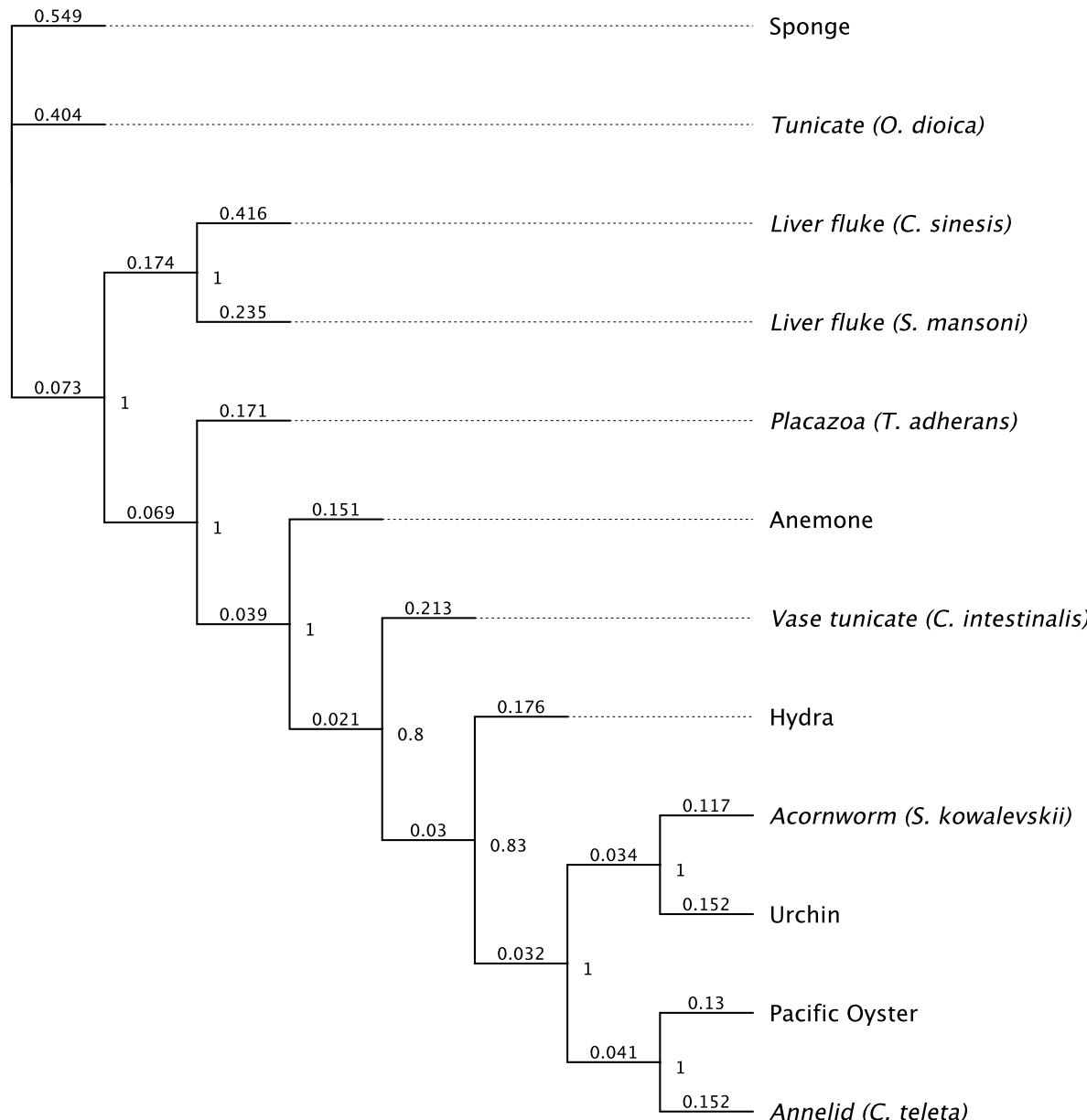
S2a Mammal Ancestor. A MrBayes tree of the sequences that were included in the reconstruction of the mammal ancestor. Node values show posterior probability, branch value shows number of replacements per residue.



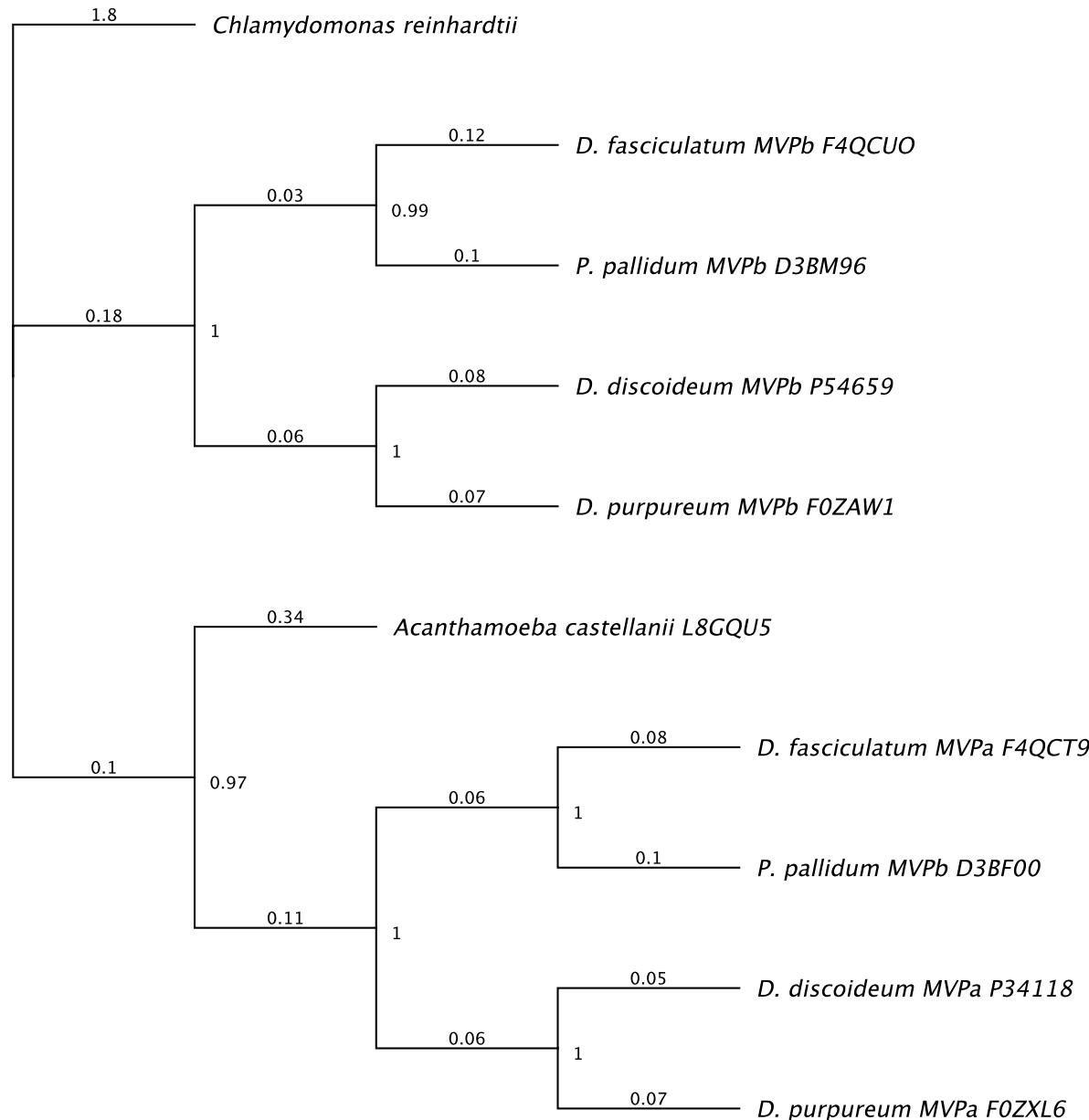
S2b Sarcopterygii Ancestor. A MrBayes tree of the sequences that were included in the reconstruction of the sarcopterygii ancestor. Node values show posterior probability, branch value shows number of replacements per residue.



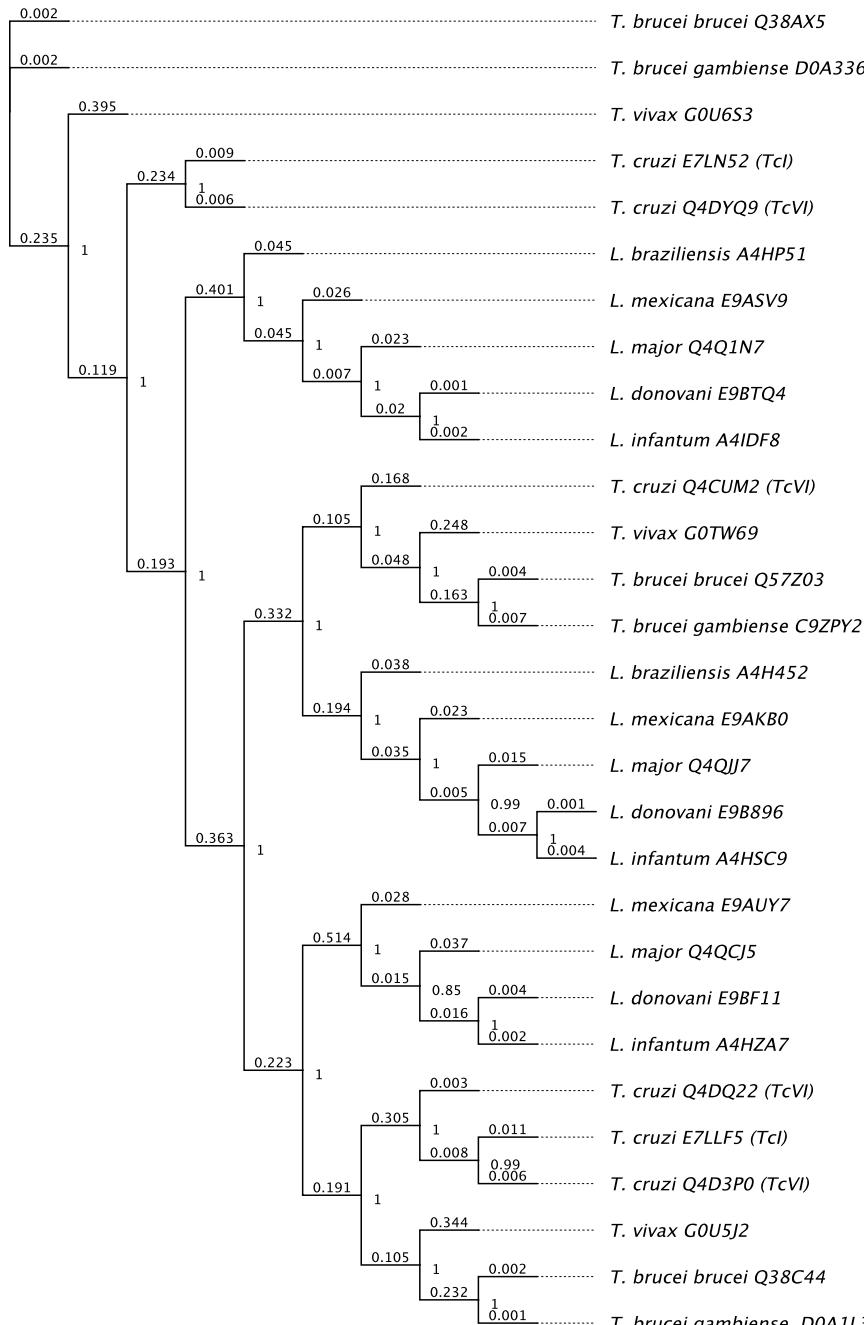
S2c Fish Ancestor. A MrBayes tree of the sequences that were included in the reconstruction of the fish ancestor. Node values show posterior probability, branch value shows number of replacements per residue.



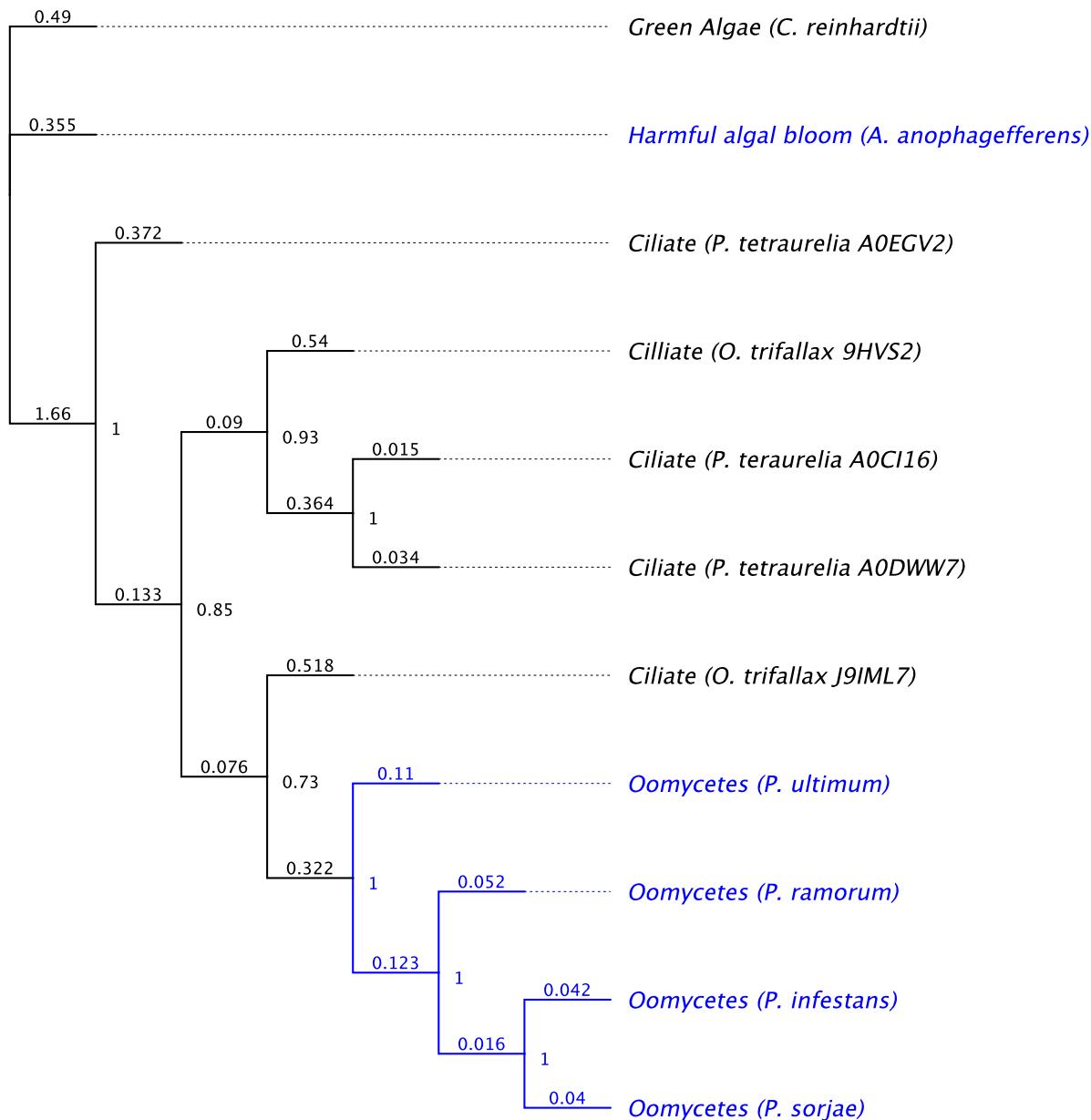
S2d Invertebrate Ancestor. A MrBayes tree of the sequences that were included in the reconstruction of the invertebrate ancestor. Node values show posterior probability, branch value shows number of replacements per residue.



S2e Amoebozoa Ancestor. A MrBayes tree of the sequences that were included in the reconstruction of the amoebozoan ancestor, rooted by *C. reinhardtii* (not included in ancestor) as in fig 2. Ancestors were made of MVP α and MVP β sequences separately. Additionally an overall amoebozoan ancestor was made from all of the sequences. The overall ancestor was more successfully docked in RosettaDock. Node values show posterior probability, branch value shows number of replacements per residue. Note that *P. pallidum* (D3BF00) is mis-annotated as both proteins from *P. pallidum* are designated MVPb.



S2f Kinetoplast Ancestor. A MrBayes tree of the sequences that were included in the reconstruction of the kinetoplast ancestor. Ancestors were constructed separately for leishmania and trypanosomes but the relationship shown by these sequences indicates that they are the result of a number of duplications prior to separation. This tree was run with a variety of out-groups to root the tree, but the complex nature of relationship is sustained. Node values show posterior probability, branch value shows number of replacements per residue.



S2g Alveolate and Stramenopile Ancestors. A MrBayes tree of the sequences that were included in the reconstruction of the alveolate (black font) and stramenopile (blue) ancestors. These were done individually and together to get an ancestor of Chromista (there were no homologous sequences or structures found in Rhizaria). Note that the HAB *A. anophagefferens* has greater homology with the green algae used as the root of the tree (not included in the ancestors), than with the other stramenopiles. Node values show posterior probability, branch value shows number of replacements per residue.